

### IN THE CLAIMS

Kindly enter the following amendments to claim 1:

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- C2
1. (amended) A method for identifying a transcribed region of interest of a genome comprising:
    - a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and
    - b) Identifying said transcribed region as a region of said genome where hybridization of all consecutive probes targeting said region are above a threshold value.
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### **REMARKS**

Applicant has amended Claim 1. Support for the amendment for claim 1 is found throughout the application and is particularly found on page 7, lines 18-25 and page 8, lines 1-3.

Applicant respectfully request reconsideration of the pending rejection and reexamination of the present claims in light of the amendments and the remarks detailed below. It is submitted that no new matter has been introduced by the present amendments and entry of the same is respectfully requested.

By these amendments, the Applicant does not acquiesce to the propriety of any of the Examiner's rejections and do not disclaim any subject matter to which Applicant are entitled.

#### ***Election/Restriction***

Applicants acknowledge the election of Group I, claims 1-9 which are being considered by the Examiner.

#### ***Specification***

The Examiner has objected to the title of the invention because the title is allegedly not descriptive. Applicants have replaced the title of the specification to "Methods for Identifying Transcribed Regions Of A Genome."

The Examiner has objected to the drawings because the figures allegedly do not conform to the margin requirements. Applicants have submitted new drawings which conform to drawing specifications.

***Rejection Under 35 U.S.C. § 112, Second Paragraph***

Claims 1-9 are rejected under 35 U.S.C. 112, second paragraph, as being allegedly indefinite for failing to particularly point and distinctly claim the subject matter which Applicant regards as the invention. Applicants respectfully disagree. However, for the purpose of expediting the issuance of claims, Applicants have amended Claim 1 to recite "A method for identifying transcribed region of interest of a genome." Additionally, Claim 6 had been rejected because there was allegedly no antecedent basis for "sub-region." Applicants respectfully disagree. Claim 6 in its first line recites "a sub-region." Therefore these rejections are obviated.

***Prior Art Rejection Under 35 U.S.C. §102***

Claims 1-3 are rejected under 35 U.S.C. §102 as being allegedly anticipated by Leary *et. al.* (US WO 99/67422). Applicants respectfully traverse the rejection.

Leary *et. al.* discusses labeling test transcripts in a detectable manner, placing the labeled test transcripts in contact with a high density grid, removing any unhybridized test transcripts from the surface of high density grid, detecting ordered positions on the high density grid, and analyzing the patterns in which the labeled test transcripts have hybridized to the genomic subfragments on the high density grid.

On the other hand, the rejected claims are directed to a method for identifying a candidate transcribed region of a genome by identifying the transcribed invention as a region of the genome where hybridization of all consecutive probes targeting the region are above a threshold value. Leary *et. al.* does not discuss identifying a transcribed region where hybridization of all consecutive probes targeting are above a threshold value. Since Leary *et. al.* does not teach every element of the claimed invention, this rejection should be withdrawn.

***Obviousness Rejection Under 35 U.S.C. §103(a)***

The Examiner has rejected claims 1-9 under 35 U.S.C. § 103(a) as being allegedly unpatentable over Leary et. al. (WO 99/67422) in Lockhart et. al. (US Patent No. 6,040,138). Applicants respectfully traverse the rejection.

The rejected claims are directed to a method for identifying a candidate transcribed region of a genome by hybridizing a plurality of nucleic acid probes with a nucleic sample wherein the nucleic sample comprises transcripts from the genome wherein the probes are targeting an area of the genome and identifying the transcribed region where hybridization of all consecutive probes are targeting a region are above a threshold value.

Leary et. al. discusses a mapping position of an individual transcript by attaching overlapping subfragments to a high density grid , preparing and labeling transcripts, hybridizing the transcripts to the subfragments, and analyzing the pattern. Leary et. al. does not discuss the hybridization of all consecutive probes are targeting a region are above a threshold value. It does not suggest identifying the transcribed region where hybridization of all consecutive probes is targeting a region is above a threshold value. In addition, Leary et. al. only discussed the use of genomic fragments in a spotted array (Page 7, lines 7-33).

Lockhart et. al. discloses gene expression monitoring array among other things. However, The Examiner has failed to point out the cited references individually or in combination, and does not provide suggestion or motivation for the claimed invention.

For the reasons above, Applicants respectfully submit the Examiner has failed to establish a prima facie case of obviousness. This rejection should be withdrawn.

## CONCLUSION

For these reasons, Applicant believes all pending claims are now in condition for allowance and should be passed to issue. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5699.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.

If the Examiner has any questions pertaining to this application, the Examiner is requested to contact the undersigned attorney.

Respectfully submitted,



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